

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/835,922

DATE: 05/08/2001
TIME: 12:07:14

Input Set : A:\Pto.amc
Output Set: N:\CRF3\05082001\I835922.raw

#2.

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2 <110> APPLICANT: Zhang, Fang L.
3   Luo, Lin
4   Gustafson, Eric
5   Liu, Yan-Hui
6   Chen, Guodong
8 <120> TITLE OF INVENTION: G-Protein Coupled Receptor and Methods
10 <130> FILE REFERENCE: CN01167K
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/835,922
C--> 13 <141> CURRENT FILING DATE: 2001-04-16
15 <150> PRIOR APPLICATION NUMBER: US 60/199,041
16 <151> PRIOR FILING DATE: 2000-04-21
18 <160> NUMBER OF SEQ ID NOS: 2
20 <170> SOFTWARE: PatentIn Ver. 2.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1187
24 <212> TYPE: DNA
25 <213> ORGANISM: homo sapiens
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (107)..(1132)
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34 cattcaaac ctccagaatc aacagttatc aggtaaccaa caagaa atg caa gcc 115
35                                     Met Gln Ala
36                                     1
38 gtc gac aat ctc acc tct gcg cct ggg aac acc agt ctg tgc acc aga 163
39 Val Asp Asn Leu Thr Ser Ala Pro Gly Asn Thr Ser Leu Cys Thr Arg
40   5 10 15
42 gac tac aaa atc acc cag gtc ctc ttc cca ctg ctc tac act gtc ctg 211
43 Asp Tyr Lys Ile Thr Gln Val Leu Phe Pro Leu Leu Tyr Thr Val Leu
44 20 25 30 35
46 ttt ttt gtt gga ctt atc aca aat ggc ctg gcg atg agg att ttc ttt 259
47 Phe Phe Val Gly Leu Ile Thr Asn Gly Leu Ala Met Arg Ile Phe Phe
48   40 45 50
50 caa atc cgg agt aaa tca aac ttt att att ttt ctt aag aac aca gtc 307
51 Gln Ile Arg Ser Lys Ser Asn Phe Ile Ile Phe Leu Lys Asn Thr Val
52   55 60 65
54 att tct gat ctt ctc atg att ctg act ttt cca ttc aaa att ctt agt 355
55 Ile Ser Asp Leu Leu Met Ile Leu Thr Phe Pro Phe Lys Ile Leu Ser
56   70 75 80
58 gat gcc aaa ctg gga aca gga cca ctg aga act ttt gtg tgt caa gtt 403
59 Asp Ala Lys Leu Gly Thr Gly Pro Leu Arg Thr Phe Val Cys Gln Val
60   85 90 95
62 acc tcc gtc ata ttt tat ttc aca atg tat atc agt att tca ttc ctg 451
63 Thr Ser Val Ile Phe Tyr Phe Thr Met Tyr Ile Ser Ile Ser Phe Leu
64 100 105 110 115
66 gga ctg ata act atc gat cgc tac cag aag acc acc agg cca ttt aaa 499

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67 Gly Leu Ile Thr Ile Asp Arg Tyr Gln Lys Thr Thr Arg Pro Phe Lys
68      120      125      130
70 aca tcc aac ccc aaa aat ctc ttg ggg gct aag att ctc tct gtt gtc 547
71 Thr Ser Asn Pro Lys Asn Leu Leu Gly Ala Lys Ile Leu Ser Val Val
72      135      140      145
74 atc tgg gca ttc atg ttc tta ctc tct ttg cct aac atg att ctg acc 595
75 Ile Trp Ala Phe Met Phe Leu Leu Ser Leu Pro Asn Met Ile Leu Thr
76      150      155      160
78 aac agg cag ccg aga gac aag aat gtg aag aaa tgc tct ttc ctt aaa 643
79 Asn Arg Gln Pro Arg Asp Lys Asn Val Lys Lys Cys Ser Phe Leu Lys
80      165      170      175
82 tca gag ttc ggt cta gtc tgg cat gaa ata gta aat tac atc tgt caa 691
83 Ser Glu Phe Gly Leu Val Trp His Glu Ile Val Asn Tyr Ile Cys Gln
84 180      185      190      195
86 gtc att ttc tgg att aat ttc tta att gtt att gta tgt tat aca ctc 739
87 Val Ile Phe Trp Ile Asn Phe Leu Ile Val Ile Val Cys Tyr Thr Leu
88      200      205      210
90 att aca aaa gaa ctg tac cgg tca tac gta aga acg agg ggt gta ggt 787
91 Ile Thr Lys Glu Leu Tyr Arg Ser Tyr Val Arg Thr Arg Gly Val Gly
92      215      220      225
94 aaa gtc ccc agg aaa aag gtg aac gtc aaa gtt ttc att atc att gct 835
95 Lys Val Pro Arg Lys Lys Val Asn Val Lys Val Phe Ile Ile Ala
96      230      235      240
98 gta ttc ttt att tgt ttt gtt cct ttc cat ttt gcc cga att cct tac 883
99 Val Phe Phe Ile Cys Phe Val Pro Phe His Phe Ala Arg Ile Pro Tyr
100      245      250      255
102 acc ctg agc caa acc cgg gat gtc ttt gac tgc act gct gaa aat act 931
103 Thr Leu Ser Gln Thr Arg Asp Val Phe Asp Cys Thr Ala Glu Asn Thr
104 260      265      270      275
106 ctg ttc tat gtg aaa gag agc act ctg tgg tta act tcc tta aat gca 979
107 Leu Phe Tyr Val Lys Glu Ser Thr Leu Trp Leu Thr Ser Leu Asn Ala
108      280      285      290
110 tgc ctg gat ccg ttc atc tat ttt ttc ctt tgc aag tcc ttc aga aat 1027
111 Cys Leu Asp Pro Phe Ile Tyr Phe Phe Leu Cys Lys Ser Phe Arg Asn
112      295      300      305
114 tcc ttg ata agt atg ctg aag tgc ccc aat tct gca aca tct ctg tcc 1075
115 Ser Leu Ile Ser Met Leu Lys Cys Pro Asn Ser Ala Thr Ser Leu Ser
116      310      315      320
118 cag gac aat agg aaa aaa gaa cag gat ggt ggt gac cca aat gaa gag 1123
119 Gln Asp Asn Arg Lys Lys Glu Gln Asp Gly Gly Asp Pro Asn Glu Glu
120      325      330      335
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123 Thr Pro Met
124 340
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130 <211> LENGTH: 342
131 <212> TYPE: PRT
132 <213> ORGANISM: homo sapiens

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134 <400> SEQUENCE: 2

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139           20           25           30
141 Thr Val Leu Phe Phe Val Gly Leu Ile Thr Asn Gly Leu Ala Met Arg
142           35           40           45
144 Ile Phe Phe Gln Ile Arg Ser Lys Ser Asn Phe Ile Ile Phe Leu Lys
145           50           55           60
147 Asn Thr Val Ile Ser Asp Leu Leu Met Ile Leu Thr Phe Pro Phe Lys
148           65           70           75           80
150 Ile Leu Ser Asp Ala Lys Leu Gly Thr Gly Pro Leu Arg Thr Phe Val
151           85           90           95
153 Cys Gln Val Thr Ser Val Ile Phe Tyr Phe Thr Met Tyr Ile Ser Ile
154           100          105          110
156 Ser Phe Leu Gly Leu Ile Thr Ile Asp Arg Tyr Gln Lys Thr Thr Arg
157           115          120          125
159 Pro Phe Lys Thr Ser Asn Pro Lys Asn Leu Leu Gly Ala Lys Ile Leu
160           130          135          140
162 Ser Val Val Ile Trp Ala Phe Met Phe Leu Leu Ser Leu Pro Asn Met
163 145          150          155          160
165 Ile Leu Thr Asn Arg Gln Pro Arg Asp Lys Asn Val Lys Lys Cys Ser
166           165          170          175
168 Phe Leu Lys Ser Glu Phe Gly Leu Val Trp His Glu Ile Val Asn Tyr
169           180          185          190
171 Ile Cys Gln Val Ile Phe Trp Ile Asn Phe Leu Ile Val Ile Val Cys
172           195          200          205
174 Tyr Thr Leu Ile Thr Lys Glu Leu Tyr Arg Ser Tyr Val Arg Thr Arg
175           210          215          220
177 Gly Val Gly Lys Val Pro Arg Lys Lys Val Asn Val Lys Val Phe Ile
178 225          230          235          240
180 Ile Ile Ala Val Phe Phe Ile Cys Phe Val Pro Phe His Phe Ala Arg
181           245          250          255
183 Ile Pro Tyr Thr Leu Ser Gln Thr Arg Asp Val Phe Asp Cys Thr Ala
184           260          265          270
186 Glu Asn Thr Leu Phe Tyr Val Lys Glu Ser Thr Leu Trp Leu Thr Ser
187           275          280          285
189 Leu Asn Ala Cys Leu Asp Pro Phe Ile Tyr Phe Phe Leu Cys Lys Ser
190           290          295          300
192 Phe Arg Asn Ser Leu Ile Ser Met Leu Lys Cys Pro Asn Ser Ala Thr
193 305          310          315          320
195 Ser Leu Ser Gln Asp Asn Arg Lys Lys Glu Gln Asp Gly Gly Asp Pro
196           325          330          335
198 Asn Glu Glu Thr Pro Met
199           340

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VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Application Number

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date